[CLAIMS]

[Claim 1]

A method for detecting a mutation, comprising:

a) amplifying a target polynucleotide using a forward primer and a reverse primer;

b) generating fragments of two or more single-stranded polynucleotides including one or more mutation sequences having the size of 2-32 bases by cleaving the amplified polynucleotide with restriction enzymes; and

c) measuring the molecular weight of the cleaved fragments.

[Claim 2]

The method according to claim 1, wherein the polynucleotide is cleaved to include one mutation among two or more different mutations in only one single stranded polynucleotide fragment and all mutations in the other single stranded nucleotide fragment.

[Claim 3]

A method for detecting a mutation, comprising:

a) amplifying a target polynucleotide using a forward primer and a reverse primer;

b) cleaving the amplified target polynucleotide by restriction enzymes wherein the second restriction enzyme does not react while a first restriction enzyme is reacted with the amplified polynucleotide; and

c) measuring the molecular weight of the cleaved fragments.

[Claim 4]

The method according to claim 1 or 3, wherein the forward primer comprises a primer binding sequence 1, a restriction enzyme recognition sequence and a primer binding sequence 2.

[Claim 5]

The method according to claim 4, wherein the forward primer is a primer selected from the group consisting of SEQ ID NO: 2, 7, 12, 20, 25 and 30.

[Claim 6]

The method according to claim 1 or 3, wherein the restriction enzyme treatments step is performed using restriction enzymes having different optimum temperatures.

[Claim 7]

The method according to claim 6, wherein the restriction enzymes are a restriction enzyme having a low optimum temperature selected from the group consisting of Fok1, Bbv I, Bsg I, Bcg I, Bpm I, BseR I and Bae I, and a restriction enzyme having a high optimum temperature selected from the group consisting of BstF5 I, Taq I, BsaB I, Btr I, BstAP I, Fau I, Bcl I, Pci I and Apo I.

[Claim 8]

The method according to claim 3, wherein the fragments cleaved by the restriction enzymes comprises a mutation sequence

[Claim 9]

The method according to claim 3 or 8, wherein the fragment cleaved by the restriction enzymes has the size of bases ranging from 2 to 32

[Claim 10]

The method according to claim 1 or 3, wherein the amplified polynucleotide

comprises a tyrosine-methionine-aspartate-aspartate (YMDD) site which is an active site of DNA polymerase of hepatitis B virus.

[Claim 11]

The method according to claim 1 or 3, wherein the amplified polynucleotide comprises 5'-NCR (non-coding region) site of a hepatitis C virus.

[Claim 12]

The method according to claim 1 or 3, wherein wherein the amplified polynucleotide comprises the 2741^{st} or 3597^{th} base site of the 4^{th} intron of a human maspin gene

[Claim 13]

A primer for analyzing a gene mutation comprising a primer binding sequence 1, a restriction enzyme recognition sequence and a primer binding sequence, wherein a polynucleotide fragment cleaved by two or more restriction enzymes for recognizing the restriction enzyme recognition sequence comprises a mutation sequence, and the polynucleotide fragment has the size of bases ranging from 2 to 32.

[Claim 14]

The primer according to claim 13, wherein the forward primer is a primer selected from the group consisting of SEQ ID NO: 2, 7, 12, 20, 25 and 30.

[Claim 15]

The primer according to claim 13, wherein the restriction enzymes have same or different optimum temperatures.

[Claim 16]

The primer according to claim 13 or 15, wherein the restriction enzymes have

different optimum temperatures.

[Claim 17]

The primer according to claim 16, wherein the restriction enzymes are a restriction enzyme having a low optimum temperature selected from the group consisting of Fok1, Bbv I, Bsg I, Bcg I, Bpm I, BseR I and Bae I, and a restriction enzyme having a high optimum temperature selected from the group consisting of BstF5 I, Taq I, BsaB I, Btr I, BstAP I, Fau I, Bcl I, Pci I and Apo I.

[Claim 18]

The primer according to claim 13 or 14, wherein the primer is used for mutation analysis of the 2741st or 3597th base site of the 4th intron of human maspin gene or for genotypic mutation analysis of lamivudine resistant hepatitis B virus or hepatitis C virus.